

seqlist.txt

SEQUENCE LISTING

<110> ERTL, Peter F.

<120> Vaccine

<130> PG5024

<140> Not Yet Assigned

<141> 2005-05-04

<150> PCT/EP2003/012429

<151> 2003-03-11

<150> GB 0225786.3

<151> 2002-11-05

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Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys	Ala	Tyr	Asp	Thr	Glu	Val
		50				55					60				
His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val	Pro	Thr	Asp	Pro	Asn	Pro
65					70					75				80	
Gln	Glu	Val	Val	Leu	Gly	Asn	Val	Thr	Glu	Tyr	Phe	Asn	Met	Trp	Lys
				85					90					95	
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Lys	Asn	Lys	Thr	Thr	Arg	Asn	Phe	Arg	Leu	Ile	His	Cys	Asn	Ser	Ser
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Val	Met	Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe	Glu	Pro	Ile	Pro	Ile
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His	Tyr	Cys	Ala	Pro	Ala	Gly	Phe	Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys
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			260					265					270		
Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	Ile	Arg	Ser	Asp	Asn	Phe	Met	Asp
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Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile	His	Ile	Gly	Pro
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			325						330					335	
Ala	His	Cys	Asn	Leu	Ser	Arg	Ala	Gln	Trp	Asn	Asn	Thr	Leu	Lys	Gln
			340					345					350		
Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys	Thr	Ile	Lys	Phe
		355					360					365			
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Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln	Leu	Phe	Asn	Ser
385					390					395					400
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Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln	Ile	Arg	Cys	Ser
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	450					455					460				
Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro	Gly	Gly	Gly	Asp
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Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Lys
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acctggaacg	gcaccgaggg	caacaacaca	gagggaaact	ccactatcac	cctcccctgc	1260
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tacaaggcag	ctgtagatct	tagccacttt	ttaaaagaaa	aggggggact	ggaagggtta	300
attcactccc	aacgaagaca	agatatcctt	gatctgtgga	tctaccacac	acaaggctac	360
ttccctgatt	ggcagaacta	cacaccaggg	ccaggggtca	gatatccact	gacccttgga	420
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seqlist.txt

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tgccaagttt gtttcataac agctgcctta ggcattctct atggcaggaa gaagcggaga 780
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			20					25					30		
Ala	Ser	Arg	Asp	Leu	Glu	Lys	His	Gly	Ala	Ile	Thr	Ser	Asn	Thr	
			35				40					45			
Ala	Ala	Thr	Asn	Ala	Ala	Cys	Ala	Trp	Leu	Glu	Ala	Gln	Glu	Glu	Glu
	50					55					60				
Glu	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met	Thr
65					70					75				80	
Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly	Gly
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Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp	Leu
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Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
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145					150					155					160
Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp	Pro
			165						170					175	
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His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys	Thr	Ser
		195					200						205		
Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	Gly	Ser	Gln
	210					215					220				
Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys	Phe	His
				230						235					240
Cys	Gln	Val	Cys	Phe	Ile	Thr	Ala	Ala	Leu	Gly	Ile	Ser	Tyr	Gly	Arg
			245						250					255	
Lys	Lys	Arg	Arg	Gln	Arg	Arg	Arg	Pro	Pro	Gln	Gly	Ser	Gln	Thr	His
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 <223> HIV-1 trNef-Tatm fusion

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seqlist.txt

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cgaagacaag atattccttga tctgtggatc taccacacac aaggctactt ccctgattgg 180
cagaactaca caccagggcc aggggtcaga tatccactga cttttggatg gtgctacaag 240
ctagtaccag ttgagccaga taaggtagaa gaggccaata aaggagagaa caccagcttg 300
ttacaccctg tgagcctgca tggaatggat gaccctgaga gagaagtgtt agagtggagg 360
tttgacagcc gcctagcatt tcatcacgtg gcccgagagc tgcattccgga gtacttcaag 420
aactgcacta gtgagccagt agatccctaga ctagagccct ggaagcatcc aggaagtcag 480
cctaaaactg cttgtaccaa ttgctattgt aaaaagtgtt gctttcattg ccaagtttgt 540
ttcataacag ctgccttagg catctcctat ggcaggaaga agcggagaca gcgacgaaga 600
cctcctcaag gcagtcagac tcatcaagtt tctctatcaa agcaaccac ctcccaatcc 660
aaaggggagc cgacaggccc gaaggaataa 690
```

<210> 54
 <211> 229
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HIV-1 trNef-Tatm fusion

```
<400> 54
Met Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
1 5 10 15
Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
20 25 30
Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
35 40 45
Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
50 55 60
Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
65 70 75 80
Leu Val Pro Val Glu Pro Asp Lys Val Glu Ala Asn Lys Gly Glu
85 90 95
Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro
100 105 110
Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
115 120 125
His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser
130 135 140
Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln
145 150 155 160
Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His
165 170 175
Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg
180 185 190
Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His
195 200 205
Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro
210 215 220
Thr Gly Pro Lys Glu
225
```

<210> 55
 <211> 1461
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HIV-1 ds-gp120c

```
<400> 55
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accaccctct tctgcgcgag cgacgccaaag gcctacgaca cggaagtgca taacgtgtgg 120
gcgacgcctg cttgcgtgcc tacggacccc aaccccagg aggtggtgct gggaaaacgtg 180
accgagtact tcaacatgtg gaagaataac atggtggatc agatgcacga ggacatcatc 240
tctctgtggg accagtcctt gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300
gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360
gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420
```

seqlist.txt

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aaggtgcaga aggaatacgc gctgttttat aatctcgatg tgggtcccat cgacgacgac 480
aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540
gtcatgacgc aggcctgccc caaggtgtcc ttcgaaccaa tcccgatcca ttactgtgcc 600
cctgccggat tcgcgatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660
accaacgtca gcacgggtgca gtgcacccat ggcacccgcc ccgtcgtgag caccagctg 720
ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780
aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840
aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgcccgc 900
aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcca gtggaataac 960
accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020
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ttcttctact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggcaac 1140
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aacgagacgg agatcttcag gcccgcgggc ggcgacatga gggataactg gcggagcgag 1380
ctgtacaagt acaagggtgg gaaggtggag ccgctcggcg tggcccccac ccgggccaag 1440
cgccgcgtcg tgcagagatg a

```

<210> 56

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c

<400> 56

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
1      5      10      15
Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65      70      75      80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145      150      155      160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225      230      235      240
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260      265      270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305      310      315      320

```

seqlist.txt

```

Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
      325      330
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
      340      350
His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
      355      360      365
Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly
      370      375      380
Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met
      385      390      395
Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln
      405      410      415
Ile Arg Cys Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
      420      425      430
Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro
      435      440      445
Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
      450      455      460
Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys
      465      470      475      480
Arg Arg Val Val Gln Arg
      485

```

<210> 57
 <211> 2340
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HIV-1 ds-gp120c'

```

<400> 57
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gcgacgcatg cttgcgtgcc tacggacccc aacccccagg aggtggtgct gggaaacgtg 180
accgagtact tcaacatgtg gaagaataac atgggtggatc agatgcacga ggacatcatc 240
tctctgtggg accagtcctt gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300
gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360
gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420
aaggtgcaga aggaatacgc gctgttttat aatctcgaat tggtcccatc cgacgacgac 480
aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540
gtcatgacgc aggcctgccc caaggtgtcc ttccaaccaa tcccgatcca ttactgtgcc 600
cctgcccgat tcgcatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660
accaacgtca gcacggtgca gtgcacccat ggcattccgc ccgtcgtgag caccagctg 720
ctgtctgaac ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780
aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840
aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgccgc 900
aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcca gtggaataac 960
accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020
aatcagagtt ctggcggaga ccccgagatc gtgcggcact ccttcaactg cggggcgag 1080
ttcttctact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggcaac 1140
aacacagagg gaaactccac tatcaccctc ccttgccgca tcaagcagat catcaacatg 1200
tggcaggagg tgggaaaggc catgtatgcc ccccccacgc ggggccagat ccgctgctcc 1260
tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
aacgagacgg agatcttcag gcccggcggc ggcgacatga gggataactg gcggagcgag 1380
ctgtacaagt acaagggtgg gaaggtggag ccgctcggcg tggcccccac ccgggccaag 1440
cgccgcgtcg tgcagagaat ggggtggcaag ttggtcaaaa gtagtgtggg tggatggcct 1500
actgtaaggg aaagaatgag acgagctgag ccagcagcag atgggggtgg agcagcatct 1560
cgagacctgg aaaaacatgg agcaatcaca agtagcaata cagcagctac caatgctgct 1620
tgtgcctggc tagaagcaca agaggaggag gaggtgggtt ttccagtcac acctcaggta 1680
cctttaagac caatgactta caaggcagct gtagatctta gccacttttt aaaagaaaag 1740
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taccacacac aaggctactt ccctgattgg cagaactaca caccagggcc aggggtcaga 1860
tatccactga cctttggatg gtgtacaag ctagtaccag ttgagccaga taaggtagaa 1920
gaggccaata aaggagagaa caccagcttg ttacaccctg tgagcctgca tggaatggat 1980
gaccctgaga gagaagtgtt agagtggagg tttgacagcc gcctagcatt tcatcacgtg 2040
gcccagagagc tgcattccga gtacttcaag aactgcacta gtgagccagt agatcctaga 2100

```

seqlist.txt

ctagagccct ggaagcatcc aggaagtcag cctaaaactg cttgtaccaa ttgctattgt 2160
 aaaaagtgtt gctttcattg ccaagtttgt ttcataacag ctgccttagg catctcctat 2220
 ggcaggaaga agcggagaca gcgacgaaga cctcctcaag gcagtcagac tcatcaagtt 2280
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<210> 58
 <211> 779
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HIV-1 ds-gp120c'

<400> 58
 Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
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 Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
 20 25 30
 Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
 35 40 45
 Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
 50 55 60
 Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
 65 70 75 80
 Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
 85 90 95
 Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
 100 105 110
 Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
 115 120 125
 Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
 130 135 140
 Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
 145 150 155 160
 Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
 165 170 175
 Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
 180 185 190
 Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
 195 200 205
 Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
 210 215 220
 Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
 225 230 235 240
 Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
 245 250 255
 Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
 260 265 270
 Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
 275 280 285
 His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
 290 295 300
 Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
 305 310 315 320
 Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
 325 330 335
 Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
 340 345 350
 His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
 355 360 365
 Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly
 370 375 380
 Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met
 385 390 395 400
 Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln
 405 410 415
 Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Thr Arg Asp Gly

Sequence												Context						
Gly	Thr	Glu	420	Gly	Asn	Gly	Thr	Glu	425	Asn	Glu	Thr	Glu	Ile	430	Phe	Arg	Pro
Gly	Gly	435	Gly	Asp	Met	Arg	Asp	440	Asn	Trp	Arg	Ser	Glu	445	Leu	Tyr	Lys	Tyr
Lys	Val	Val	Lys	Val	Glu	470	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys	480	Val
Arg	Arg	Val	Val	Gln	485	Arg	Met	Gly	Gly	Lys	490	Trp	Ser	Lys	Ser	495	Ser	Val
Val	Gly	Trp	Pro	Thr	Val	Arg	Glu	Arg	505	Met	Arg	Arg	Ala	Glu	Pro	Ala	510	Ala
Ala	Asp	Gly	Val	Gly	Ala	Ala	Ser	520	Arg	Asp	Leu	Glu	Lys	525	His	Gly	Ala	Ala
Ile	Thr	Ser	Ser	Asn	Thr	Ala	535	Ala	Thr	Asn	Ala	Ala	540	Cys	Ala	Trp	Leu	Leu
Glu	Ala	Gln	Glu	Glu	Glu	550	Glu	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	560	Val
Pro	Leu	Arg	Pro	Met	565	Thr	Tyr	Lys	Ala	Ala	570	Val	Asp	Leu	Ser	His	575	Phe
Leu	Lys	Glu	Lys	Gly	Gly	Leu	Glu	Gly	585	Leu	Ile	His	Ser	Gln	Arg	Arg	590	Arg
Gln	Asp	Ile	Leu	Asp	Leu	Trp	Ile	600	Tyr	His	Thr	Gln	Gly	605	Tyr	Phe	Pro	Pro
Asp	Trp	Gln	Asn	Tyr	Thr	Pro	615	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	620	Thr
Phe	Gly	Trp	Cys	Tyr	Lys	630	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	640	Glu
Glu	Ala	Asn	Lys	Gly	Glu	Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	655	Leu	660	Leu
His	Gly	Met	Asp	Asp	Pro	Glu	Arg	Glu	665	Val	Leu	Glu	Trp	Arg	Phe	Asp	670	Asp
Ser	Arg	Leu	Ala	Phe	His	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	680	685	Tyr
Phe	Lys	Asn	Cys	Thr	Ser	Glu	695	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	700	Trp
Lys	His	Pro	Gly	Ser	Gln	710	Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	720	Cys
Lys	Lys	Cys	Cys	Phe	His	Cys	Gln	Val	Cys	Phe	Ile	Thr	Ala	Ala	735	Leu	740	Leu
Gly	Ile	Ser	Tyr	Gly	Arg	Lys	Lys	Arg	745	Arg	Gln	Arg	Arg	Arg	750	Pro	Pro	Pro
Gln	Gly	Ser	Gln	Thr	His	Gln	Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser	765	770	Ser
Gln	Ser	Lys	Gly	Glu	Pro	Thr	775	Gly	Pro	Lys	Glu							

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<210> 59
<211> 2148
<212> DNA
<213> Artificial sequence
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<220>
<223> HIV-1 ds-gp120c trNef-Tatm fusion

<400>	59						
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accagtgact	tcaacatgtg	gaagaataac	atggtggatc	agatgcacga	ggacatcatc	240	
tctctgtggg	accagtcctt	gaagccctgc	gtgaagctga	cgctctctg	cgtgacactg	300	
gactgtgacg	acgtcaacac	caccaacagc	actaacacca	ccagcaacgc	ctggaccgga	360	
gagattcgga	agggcgcgat	caagaatact	tccttcaata	tcacgacctc	gatcacagac	420	
aagggtcgaga	aggaatacgc	gctgttttat	aatctcgtat	tgggtcccat	cgacgcagac	480	
aatgccacca	ccaagaacaa	gacgacgcgt	aatttcagac	tcattcactg	caacagcagc	540	
gtcatgacgc	aggcctgtcc	caaggtgtcc	ttcgaaccaa	tcccgatcca	ttactgtgcc	600	
cctgccggat	tcgcgatctt	caagtgtaac	aacaagacct	tcgacgggaa	gggctgtg	660	
accaacgtca	qcacggtgca	gtgcacccat	ggcatccgcc	ccgtcgtgag	caccacgctg	720	

seqlist.txt

```

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aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcca gtggaataac 960
accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020
aatcagagtt ctggcgagga ccccgagatc gtgcggcact ccttcaactg cgggggcgag 1080
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cggagatgcc gacgaagac tcctcaaggc agtcagactc atcaagttt tctatcaag 2100
caaccacct cccaatccaa aggggagccg acaggcccga aggaataa 2148

```

<210> 60

<211> 715

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c trNef-Tatm fusion

<400> 60

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
1      5      10      15
Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
20     25     30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35     40     45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50     55     60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65     70     75
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
85     90     95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100    105    110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115    120    125
Asn Cys Ser Phe Asn Ile Thr Ser Ile Arg Asp Lys Val Gln Lys
130    135    140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145    150    155
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165    170    175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180    185    190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195    200    205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210    215    220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225    230    235
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245    250    255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260    265    270

```

seqlist.txt

```

Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
      275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
      290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
      305      310      315      320
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
      325      330      335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Asp Pro Glu Ile Val Arg
      340      345      350
His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
      355      360      365
Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Thr Glu Gly
      370      375      380
Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met
      385      390      395      400
Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln
      405      410      415
Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
      420      425      430
Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro
      435      440      445
Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
      450      455      460
Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys
      465      470      475      480
Arg Arg Val Val Gln Arg Met Val Gly Phe Pro Val Thr Pro Gln Val
      485      490      495
Pro Leu Arg Pro Met Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe
      500      505      510
Leu Lys Glu Lys Gly Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg
      515      520      525
Gln Asp Ile Leu Asp Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro
      530      535      540
Asp Trp Gln Asn Tyr Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr
      545      550      555      560
Phe Gly Trp Cys Tyr Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu
      565      570      575
Glu Ala Asn Lys Gly Glu Asn Thr Ser Leu Leu His Pro Val Ser Leu
      580      585      590
His Gly Met Asp Asp Pro Glu Arg Glu Val Leu Glu Trp Arg Phe Asp
      595      600      605
Ser Arg Leu Ala Phe His His Val Ala Arg Glu Leu His Pro Glu Tyr
      610      615      620
Phe Lys Asn Cys Thr Ser Glu Pro Val Asp Pro Arg Leu Glu Pro Trp
      625      630      635      640
Lys His Pro Gly Ser Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys
      645      650      655
Lys Lys Cys Cys Phe His Cys Gln Val Cys Phe Ile Thr Ala Ala Leu
      660      665      670
Gly Ile Ser Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro
      675      680      685
Gln Gly Ser Gln Thr His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser
      690      695      700
Gln Ser Lys Gly Glu Pro Thr Gly Pro Lys Glu
      705      710      715

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<210> 61

<211> 1887

<212> DNA

<213> Artificial sequence

<220>

<223> HIV-1 ds-gp120c trNef fusion

<400> 61

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seqlist.txt

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accgagtact tcaacatgtg gaagaataac atggtggatc agatgcacga ggacatcatc 240
tctctgtggg accagtcctt gaagccctgc gtgaagtga cgctctctg cgtgacactg 300
gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360
gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420
aaggtgcaga aggaatacgc gctgttttat aatctcgatg tggcccccat cgacgacgac 480
aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540
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cctgcccgat tcgcatcctt caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660
accaacgtca gcacggtgca gtgcacccat ggcattccgc ccgtcgtgag caccagctg 720
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aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840
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tggcaggagg tgggaaaggg catgtatgcc ccccccacgc ggggccagat ccgctgctcc 1260
tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
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ctgtacaagt acaaggtggg gaaggtggag ccgctcggcg tggccccac ccgggccaag 1440
cgccgcgtcg tgcagagaat ggtgggtttt ccagtcacac ctcaggtagc ttaagacca 1500
atgacttaca aggcagctgt agatcttagc cactttttta aagaaaaggg gggactggaa 1560
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ggagagaaca ccagcttgtt acaccctgtg agcctgcatg gaatggatga ccctgagaga 1800
gaagtgttag agtggagggt tgacagccgc ctagcatttc atcacgtggc ccgagagctg 1860
catccggagt acttcaagaa ctgctaa 1887

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<210> 62

<211> 628

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c trNef fusion

<400> 62

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Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
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Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
      20     25     30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
      35     40     45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
      50     55     60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
      65     70     75     80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
      85     90     95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
      100    105    110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
      115    120    125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
      130    135    140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
      145    150    155    160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
      165    170    175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
      180    185    190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
      195    200    205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser

```

seqlist.txt

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      210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225 230 235 240
Leu Leu Asn Gly Ser Leu Ala Glu Glu Val Val Ile Arg Ser Asp
245 250 255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260 265 270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Thr Arg Lys Gly Ile
275 280 285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290 295 300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305 310 315 320
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
325 330 335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
340 345 350
His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
355 360 365
Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly
370 375 380
Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met
385 390 395 400
Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln
405 410 415
Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
420 425 430
Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro
435 440 445
Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
450 455 460
Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys
465 470 475 480
Arg Arg Val Val Gln Arg Met Val Gly Phe Pro Val Thr Pro Gln Val
485 490 495
Pro Leu Arg Pro Met Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe
500 505 510
Leu Lys Glu Lys Gly Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg
515 520 525
Gln Asp Ile Leu Asp Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro
530 535 540
Asp Trp Gln Asn Tyr Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr
545 550 555 560
Phe Gly Trp Cys Tyr Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu
565 570 575
Glu Ala Asn Lys Gly Glu Asn Thr Ser Leu Leu His Pro Val Ser Leu
580 585 590
His Gly Met Asp Asp Pro Glu Arg Glu Val Leu Glu Trp Arg Phe Asp
595 600 605
Ser Arg Leu Ala Phe His His Val Ala Arg Glu Leu His Pro Glu Tyr
610 615 620
Phe Lys Asn Cys
625

```

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<210> 63
<211> 1517
<212> DNA
<213> Artificial sequence

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<220>
<223> HIV-1 Nef p17/24 fusion

```

```

<400> 63
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tgcgcccggg aggcaaaaag aaatacaagc tcaagcatat cgtgtgggcc tcgagggagc 120
ttgaacggtt tgccgtgaac ccaggcctgc tggaacatc tgagggatgt cgccagatcc 180
tggggcaatt gcagccatcc ctccagaccg ggagtgaaga gctgaggtcc ttgtataaca 240

```

seqlist.txt

```

cagtggctac cctctactgc gtacaccaga ggatcgagat taaggatacc aaggaggcct 300
tggaacaaat tgaggaggag caaaacaaga gcaagaagaa ggcccagcag gcagctgctg 360
acactgggca tagcaaccag gtatcacaga actatcctat tgtccaaaac attcagggcc 420
agatgggttca tcaggccatc agcccccgga cgctcaatgc ctgggtgaag gttgtcgaag 480
agaaggcctt ttctcctgag gttatcccca tgttctcgc tttgagttag ggggccactc 540
ctcaggacct caatacaatg cttaataaccg tgggcggcc tcaggccgcc atgcaaagt 600
tgaaggagac tatcaacgag gaggcagccg agtgggacag agtgcattccc gtccacgctg 660
gcccgaatcg gcccggagac atgcgggagc ctcgcggtc tgacattgcc ggcaccacct 720
ctacactgca agagcaaatc ggatggatga ccaacaatcc tcccatccca gttggagaaa 780
tctataaacc gtggatcatt ctcggtctca ataaaattgt tagaatgtac tctccgacat 840
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ataagacctt gcgagcagag caggcctctc aggaggtcaa aaactggatg acggagacac 960
tcctggtaca gaacgctaag cccgactgca aaacaattct gaaggcacta ggcccggctg 1020
ccaccctgga agagatgatg accgcctgtc agggagtagg cggacccgga cacaagcca 1080
gagtgttgat ggtgggtttt ccagtcacac ctgaggtacc ttttaagacca atgacttaca 1140
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ctgattggca gaactacaca ccagggccag gggtcagata tccactgacc ttggatggg 1320
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ccagcttggt acaccctgtg agcctgcatg ggatggatga cccggagaga gaagtgttag 1440
agtggaggtt tgacagccgc ctgacatttc atcacgtggc ccgagagctg catccggagt 1500
acttcaagaa ctgctga 1517

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<210> 64

<211> 2976

<212> DNA

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 trNef fusion

<400> 64

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gcgacgcatg cttgcgtgcc tacggacccc aacccccagg aggtggtgct gggaaacgtg 180
accgagtact tcaacatgtg gaagaataac atggtggatc agatgcacga ggacatcatc 240
tctctgtggg accagctccct gaagccctgc gtgaagctga cgctctctg cgtgacactg 300
gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360
gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420
aaggtgcaga aggaatacgc gctgttttat aatctcgatg tgggtccccg cgacgacgac 480
aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540
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accaacgtca gcacggtgca gtgcacccat ggcattccgc ccgtcgtgag caccagctg 720
ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780
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tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
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```

seqlist.txt

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cgagagctgc atccggagta ctcaagaac tgctaa 2976

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<210> 65
 <211> 991
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HIV-1 ds-gp120c p17/24 trNef fusion

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<400> 65
Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
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Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
 20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
 35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
 50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
 65      70      75
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
 85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145      150      155
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225      230      235
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260      265      270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305      310      315
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
325      330      335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
340      345      350

```

seqlist.txt

His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln
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Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly
	370					375					380				
Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met
385					390					395					400
Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln
			405						410					415	
Ile	Arg	Cys	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	
			420				425					430			
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro
		435					440					445			
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr
	450					455					460				
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys
465					470					475					480
Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly
				485					490					495	
Gly	Glu	Leu	Asp	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys
			500					505					510		
Lys	Lys	Tyr	Lys	Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu
		515					520					525			
Arg	Phe	Ala	Val	Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg
	530					535					540				
Gln	Ile	Leu	Gly	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu
545					550					555					560
Leu	Arg	Ser	Leu	Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln
				565					570					575	
Arg	Ile	Glu	Ile	Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu
			580					585					590		
Glu	Gln	Asn	Lys	Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr
		595					600					605			
Gly	His	Ser	Asn	Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile
	610					615					620				
Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala
625					630					635					640
Trp	Val	Lys	Val	Val	Glu	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro
				645					650					655	
Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr
			660					665					670		
Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys
		675					680					685			
Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val
	690					695					700				
His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser
705					710					715					720
Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met
				725					730					735	
Thr	Asn	Asn	Pro	Pro	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile
			740					745					750		
Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile
		755					760					765			
Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp
	770					775					780				
Arg	Phe	Tyr	Lys	Thr	Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys
785					790					795					800
Asn	Trp	Met	Thr	Glu	Thr	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys
				805					810					815	
Lys	Thr	Ile	Leu	Lys	Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met
			820					825					830		
Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val
		835					840					845			
Leu	Met	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met
	850					855					860				
Thr	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly
865					870					875					880
Gly	Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp
				885					890					895	

seqlist.txt

Leu	Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr
			900					905					910		
Thr	Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr
		915					920					925			
Lys	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly
	930					935					940				
Glu	Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp
945				950						955				960	
Pro	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala	Phe
			965						970					975	
His	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys	
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<210> 66
 <211> 3237
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HIV-1 ds-gp120c p17/24 trNef Tatm fusion

<400> 66

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gcgacgcatt	cttgcggtgc	tacggacccc	aacccccagg	aggtggtgct	gggaaacgtg	180
accgagtact	tcaacatgtg	gaagaataac	atggtggatc	agatgcacga	ggacatcatc	240
tctctgtggg	accagtccct	gaagccctgc	gtgaagctga	cgcctctctg	ctgacactcg	300
gactgtgacg	acgtcaacac	caccaacagc	actaccacca	ccagcaacgg	ctggaccgga	360
gagattcgga	agggcgagat	caagaactgc	tccttcaata	tcacgacctc	gatcagagac	420
aaggtgcaga	aggaatacgc	gctgttttat	aatctcgaat	tggtcccat	cgacgacgac	480
aatgccacca	ccaagaacaa	gacgacgcgt	aatcttcagac	tcattcactg	caacagcagc	540
gtcatgacgc	aggcctgccc	caaggtgtcc	ttcgaaccaa	tcccgatcca	ttactgtgcc	600
cctgcccgat	tgcgcgatcct	caagtgtaac	aacaagacct	tgcacgggaa	gggcctgtgc	660
accaacgtca	gcacgggtgca	gtgcacccat	ggcatccgcc	ccgtcgtgag	cacccagctg	720
ctgctgaacg	ggtcccttggc	tgaggaggag	gtggtgatcc	ggtcggacaa	cttcattggac	780
aacaccaaga	caatcatcgt	ccagctgaac	gagctctgtg	cgattaactg	taccggcct	840
aacaacaaca	cccgtgaagg	catccacatc	gggcctggac	gggccttcta	tgccgcccgc	900
aagatcatcg	gcgacatccg	gcaggcccat	tgcaacctct	cccgcgccc	gtggaataac	960
accctgaagc	agatcgtgat	caagctgaga	gagcactttg	gaaacaagac	catcaagttc	1020
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ttcttctact	gcgatacgac	acagctcttc	aactccacct	ggaacggcac	cgagggcaac	1140
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aacgagacgg	agatcttcag	gcccggcgcc	gccgacatga	gggataactg	gcggagcgag	1380
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agaatgtact	ctccgacatc	catccttgac	attagacagg	gacccaaaga	gccttttagg	2340
gattacgtcg	accggtttta	taagaccctg	cgagcagagc	aggcctctca	ggaggtcaaa	2400
aactgtatga	cggagacata	cctggtacag	aacgctaac	ccgactgcaa	aacaatcttg	2460
aaggcactag	ggccggctgc	caccctggaa	gagatgatga	ccgcctgtca	gggagttagc	2520
ggacccggac	acaaagccag	agtgttgatg	gtgggttttc	cagtcacacc	tcaggtacct	2580
ttaagaccaa	tgacttacaa	ggcagctgta	gatcttagcc	actttttaaa	agaaaagggg	2640
ggactggaag	ggctaattca	ctcccaacga	agacaagata	tccttgatct	gtggatctac	2700

seqlist.txt

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cacacacaag gctacttccc tgattggcag aactacacac cagggccagg ggtagaatat 2760
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gccataaag gagagaacac cagcttgtaa caccctgtga gcctgcatgg aatggatgac 2880
cctgagagag aagtgttaga gtggaggttt gacagccgcc tagcatttca tcacgtggcc 2940
cgagagctgc atccggagta cttcaagaac tgcactagtg agccagtaga tcctagacta 3000
gagccctgga agcatccagg aagtcagcct aaaactgctt gtaccaattg ctattgtaaa 3060
aagtgttgct ttcattgcca agtttgtttc ataacagctg ccttaggcat ctcctatggc 3120
aggaagaagc ggagacagcg acgaagacct cctcaaggca gtcagactca tcaagtttct 3180
ctatcaaagc aaccacacct ccaatccaaa ggggagccga caggcccga ggaataa 3237

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<210> 67

<211> 1078

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 trNef Tatm fusion

<400> 67

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1      5      10     15
Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
20     25     30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35     40     45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50     55     60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65     70     75
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
85     90     95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100    105    110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115    120    125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130    135    140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145    150    155
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165    170    175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180    185    190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195    200    205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210    215    220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225    230    235
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245    250    255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260    265    270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275    280    285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290    295    300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305    310    315
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
325    330    335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
340    345    350
His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
355    360    365
Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly
370    375    380
Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met

```

seq1ist.txt

```

385      390      395      400
Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln
405      410      415
Ile Arg Cys Ser Asn Ile Thr Gly Leu Leu Thr Arg Asp Gly
420      425      430
Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro
435      440      445
Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
450      455      460
Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys
465      470      475      480
Arg Arg Val Val Gln Arg Met Gly Ala Arg Ala Ser Val Leu Ser Gly
485      490      495
Gly Glu Leu Asp Arg Trp Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys
500      505      510
Lys Lys Tyr Lys Leu Lys His Ile Val Trp Ala Ser Arg Glu Leu Glu
515      520      525
Arg Phe Ala Val Asn Pro Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg
530      535      540
Gln Ile Leu Gly Gln Leu Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu
545      550      555      560
Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln
565      570      575      580
Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu
585      590      595
Glu Gln Asn Lys Ser Lys Lys Ala Gln Gln Ala Ala Asp Thr
600      605      610
Gly His Ser Asn Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile
615      620      625
Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala
630      635      640
Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro
645      650      655
Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr
660      665      670
Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys
675      680      685
Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val
690      695      700
His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser
705      710      715      720
Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
725      730      735
Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile
740      745      750
Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile
755      760      765
Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp
770      775      780
Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys
785      790      795      800
Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys
805      810      815
Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met
820      825      830
Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val
835      840      845
Leu Met Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met
850      855      860
Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly
865      870      875      880
Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp
885      890      895
Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr
900      905      910
Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr
915      920      925
Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly

```

seqlist.txt

```

      930                      935                      940
Glu Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp
945                      950                      955                      960
Pro Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe
      965                      970                      975
His His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr
      980                      985                      990
Ser Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
      995                      1000                      1005
Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
      1010                      1015                      1020
His Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly
1025                      1030                      1035                      1040
Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
      1045                      1050                      1055
His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu
      1060                      1065                      1070
Pro Thr Gly Pro Lys Glu
1075

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<210> 68
 <211> 3429
 <212> DNA
 <213> Artificial sequence

<220>
 <223> HIV-1 ds-gp120c p17/24 Nef Tatm fusion

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<400> 68
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gcgacgcatt cttgcgtgcc tacggacccc aacccccagg aggtggtgct gggaaacgtg 180
accgagtact tcaacatgtg gaagaataac atggtggatc agatgcacga ggacatcatc 240
tctctgtggg accagtcctt gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300
gactgtgacg acgtcaaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360
gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420
aaggtgcaga aggaatacgc gctgttttat aatctcgatg tggccccat cgacgacgac 480
aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540
gtcatgacgc aggcctgccc caaggtgtcc ttccaacaa tcccgatcca ttactgtgcc 600
cctgcccgat tcgcgatacct caagtgtaac tgcacgggaa gggcctgtgc 660
accaacgtca gcacggtgca gtgcacccat ggcattccgc ccgtcgtgag caccagctg 720
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seqlist.txt

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<210> 69

<211> 1142

<212> PRT

<213> Artificial sequence

<220>

<223> HIV-1 ds-gp120c p17/24 Nef Tatm fusion

<400> 69

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Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65      70      75
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100     105     110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115     120     125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130     135     140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145     150     155
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165     170     175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180     185     190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195     200     205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210     215     220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225     230     235
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245     250     255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260     265     270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275     280     285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290     295     300

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seqlist.txt

```

Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305 310 315 320
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
325 330 335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
340 345 350
His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
355 360 365
Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Thr Glu Gly
370 375 380
Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met
385 390 395 400
Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln
405 410 415
Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
420 425 430
Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro
435 440 445
Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
450 455 460
Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys
465 470 475 480
Arg Arg Val Val Gln Arg Met Gly Ala Arg Ala Ser Val Leu Ser Gly
485 490 495
Gly Glu Leu Asp Arg Trp Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys
500 505 510
Lys Lys Tyr Lys Leu Lys His Ile Val Trp Ala Ser Arg Glu Leu Glu
515 520 525
Arg Phe Ala Val Asn Pro Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg
530 535 540
Gln Ile Leu Gly Gln Leu Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu
545 550 555 560
Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln
565 570 575
Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu
580 585 590
Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln Gln Ala Ala Asp Thr
595 600 605
Gly His Ser Asn Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile
610 615 620
Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala
625 630 635 640
Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro
645 650 655
Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr
660 665 670
Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys
675 680 685
Glu Thr Ile Asn Glu Glu Ala Glu Trp Asp Arg Val His Pro Val
690 695 700
His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser
705 710 715 720
Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
725 730 735
Thr Asn Asn Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile
740 745 750
Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile
755 760 765
Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp
770 775 780
Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys
785 790 795 800
Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys
805 810 815
Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met
820 825 830
Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val
835 840 845

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seqlist.txt

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865					870					875					880
Ala	Ala	Ser	Arg	Asp	Leu	Glu	Lys	His	Gly	Ala	Ile	Thr	Ser	Ser	Asn
				885					890					895	
Thr	Ala	Ala	Thr	Asn	Ala	Ala	Cys	Ala	Trp	Leu	Glu	Ala	Gln	Glu	Glu
			900					905					910		
Glu	Glu	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met
		915					920					925			
Thr	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly
	930					935					940				
Gly	Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp
945				950						955					960
Leu	Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr
				965					970					975	
Thr	Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr
			980					985					990		
Lys	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly
	995						1000					1005			
Glu	Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp
	1010					1015					1020				
Pro	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala	Phe
1025					1030					1035					1040
His	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys	Thr
				1045					1050					1055	
Ser	Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	Gly	Ser
			1060					1065					1070		
Gln	Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys	Phe
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<210> 70
 <211> 3426
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HIV-1 ds-gp120c p17/24 mNef Tatm fusion

<400> 70

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accctgaagc	agatcgtgat	caagctgaga	gagcactttg	gaaacaagac	catcaagttc	1020
aatcagagtt	ctggcggaga	ccccgagatc	gtgcggcact	ccttcaactg	cgggggcgag	1080
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seqlist.txt

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<210> 71

<211> 1141

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 mNef Tatm fusion

<400> 71

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Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35     40     45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50     55     60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65     70     75     80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
85     90     95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100    105    110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115    120    125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130    135    140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp

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seqlist.txt

145	Asn	Ala	Thr	Thr	Lys	150	Asn	Lys	Thr	Thr	Arg	155	Asn	Phe	Arg	Leu	Ile	160	His
					165						170						175		
Cys	Asn	Ser	Ser	Val	Met	Thr	Gln	Ala	185	Cys	Pro	Lys	Val	Ser	190	Phe	Glu		
Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	200	Pro	Ala	Gly	Phe	Ala	Ile	Leu	Lys			
		195											205						
Cys	Asn	Asn	Lys	Thr	Phe	Asp	Gly	Lys	Gly	Leu	Cys	220	Thr	Asn	Val	Ser			
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Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	Pro	Val	Val	235	Ser	Thr	Gln	Leu			
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Thr	Leu	Lys	Gln	Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys				
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His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln				
		355																	
Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly				
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Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met				
385					390														
Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln				
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Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly				
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Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro				
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Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr				
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Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys				
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Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly				
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Gly	Glu	Leu	Asp	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys				
			500					505											
Lys	Lys	Tyr	Lys	Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu				
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Arg	Phe	Ala	Val	Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg				
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Gln	Ile	Leu	Gly	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu				
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Leu	Arg	Ser	Leu	Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln				
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Glu	Gln	Asn	Lys	Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr				
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Gly	His	Ser	Asn	Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile				
		610				615													
Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala				
625					630														
Trp	Val	Lys	Val	Val	Glu	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro				
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Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr				
			660					665											
Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys				
		675					680												
Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val				

seqlist.txt

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Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile
740      745      750
Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile
755      760      765
Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp
770      775      780
Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys
785      790      795
Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys
805      810      815
Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met
820      825      830
Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val
835      840      845
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850      855      860
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865      870      875
Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr
885      890      895
Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu
900      905      910
Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
915      920      925
Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
930      935      940
Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
945      950      955
Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
965      970      975
Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
980      985      990
Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu
995      1000      1005
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1010      1015      1020
Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
1025      1030      1035
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1045      1050      1055
Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln
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Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His
1075      1080      1085
Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg
1090      1095      1100
Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His
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<210> 72

<211> 3429

<212> DNA

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 L1-Nef Tatm fusion

<400> 72

seqlist.txt

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aaggcactag gcccgctgc caccctggaa gagatgatga ccgcctgtca gggagtaggc 2520
ggacccggac acaaagccag agtgttgatg ggtggcaagt ggtcaaaaag tagtgtggtt 2580
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aaggtagaag aggccataaa aggagagaac accagcgctt tacaccctgt gagcctgcat 3060
ggaatggatg accctgagag gcatccggag gagtggaggt ttgacagccg cctagcattt 3120
catcacgtgg cccgagagct gaagcatcca tacttcaaga actgcactag tgagccagta 3180
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atctcctatg gcaggaagaa gcggagacag cgacgaagac ctcctcaagg cagtcagact 3360
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aaggaataa 3429

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<210> 73

<211> 1142

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 L1-Nef Tatm fusion

<400> 73

seqlist.txt

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 1      5      10      15
Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
 20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
 35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
 50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
 65      70      75      80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
 85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145      150      155      160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225      230      235      240
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260      265      270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305      310      315      320
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
325      330      335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
340      345      350
His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
355      360      365
Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly
370      375      380
Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met
385      390      395      400
Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln
405      410      415
Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
420      425      430
Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro
435      440      445
Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
450      455      460
Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys
465      470      475      480
Arg Arg Val Val Gln Arg Met Gly Ala Arg Ala Ser Val Leu Ser Gly
485      490      495
Gly Glu Leu Asp Arg Trp Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys
500      505      510
Lys Lys Tyr Lys Leu Lys His Ile Val Trp Ala Ser Arg Glu Leu Glu
515      520      525
Arg Phe Ala Val Asn Pro Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg
530      535      540

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seqlist.txt

Gln Ile Leu Gly Gln Leu Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu
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 Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu
 580 585 590
 Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln Gln Ala Ala Asp Thr
 595 600 605
 Gly His Ser Asn Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile
 610 615 620
 Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala
 625 630 635 640
 Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro
 645 650 655
 Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr
 660 665 670
 Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys
 675 680 685
 Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val
 690 695 700
 His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser
 705 710 715 720
 Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
 725 730 735
 Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile
 740 745 750
 Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile
 755 760 765
 Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp
 770 775 780
 Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys
 785 790 795 800
 Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys
 805 810 815
 Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met
 820 825 830
 Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val
 835 840 845
 Leu Met Gly Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr
 850 855 860
 Val Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly
 865 870 875 880
 Ala Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn
 885 890 895
 Thr Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu
 900 905 910
 Glu Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met
 915 920 925
 Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly
 930 935 940
 Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp
 945 950 955 960
 Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr
 965 970 975
 Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr
 980 985 990
 Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly
 995 1000 1005
 Glu Asn Thr Ser Ala Leu His Pro Val Ser Leu His Gly Met Asp Asp
 1010 1015 1020
 Pro Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe
 1025 1030 1035 1040
 His His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr
 1045 1050 1055
 Ser Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
 1060 1065 1070
 Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
 1075 1080 1085

seqlist.txt

His Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly
 1090 1095 1100
 Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
 1105 1110 1115 1120
 His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu
 1125 1130 1135
 Pro Thr Gly Pro Lys Glu
 1140

<210> 74
 <211> 3429
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HIV-1 ds-gp120c p17/24 L2-Nef Tatm fusion

<400> 74
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 gcgagcatg cttgcgtgcc tacggacccc aacccccagg aggtgggtgct gggaaacgtg 180
 accgagtact tcaacatgtg gaagaataac atgggtggatc agatgcacga ggacatcatc 240
 tctctgtggg accagtcctt gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300
 gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360
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 aaggtgcaga aggaatacgc gctgttttat aatctcgatg tggccccat cgacgacgac 480
 aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540
 gtcattgacg aggcctgccc caaggtgtcc ttcgaaccaa tcccgatcca ttactgtgcc 600
 cctgcccgat tcgcgatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660
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 aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgcccgc 900
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 aaagaaaagg ggggactgga agggctaatt cactcccaac gaagacaaga tatccttgat 2880
 ctgtggatct accacacaca aggtacttcc cctgattggc agaactacac accagggcc 2940

seqlist.txt

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aaggaataa

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<210> 75

<211> 1142

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 L2-Nef Tatm fusion

<400> 75

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Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
 1      5      10      15
Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
 20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
 35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
 50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
 65      70      75      80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
 85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145      150      155      160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225      230      235      240
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260      265      270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305      310      315      320
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
325      330      335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
340      345      350
His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
355      360      365
Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly
370      375      380
Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met

```

seqlist.txt

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385      390      395      400
Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln
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Ile Arg Cys Ser 420 Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro
435 Gly Thr Glu Gly Asp Met Arg Asp Asn Trp Arg Ser Glu 445 Leu Tyr Lys Tyr
450 Gly Gly Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys
465 Lys Val Val Lys Val Gln Arg Met Gly Ala Arg Ala Ser Val Leu Ser Gly
485 Gly Glu Leu Asp Arg Trp Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys
500 Lys Lys Tyr Lys Leu Lys His Ile Val Trp Ala Ser Arg 510 Glu Leu Glu
515 Arg Phe Ala Val Asn Pro Gly 520 Leu Leu Glu Thr Ser 525 Glu Cys Arg
530 Gln Ile Leu Gly Gln Leu Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu
545 Leu Arg Ser Leu Tyr 550 Asn Thr Val Ala Thr 555 Leu Tyr Cys Val His 560
565 Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu
580 Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln Gln Ala Ala Asp Thr
595 Gly His Ser Asn Gln Val Ser 600 Gln Asn Tyr Pro Ile Val Gln Asn Ile
610 Gln Gly Gln Met Val His 615 Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala
625 Trp Val Lys Val Val 630 Glu Glu Lys Ala Phe 635 Ser Pro Glu Val Ile 640
645 Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr
660 Met Leu Asn Thr Val Gly Gly His 665 Gln Ala Ala Met Gln Met Leu Lys
675 Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val
690 His Ala Gly Pro Ile Ala 695 Pro Gly Gln Met Arg Glu Pro Arg Gly Ser
705 Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
725 Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile
740 Ile Leu Gly Leu Asn Lys Ile Val 745 Arg Met Tyr Ser Pro Thr Ser Ile
755 Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp
770 Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys
785 Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys
805 Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Met
820 Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val
835 Leu Met Gly Gly Lys Trp Ser 840 Lys Ser Ser Val Val Gly Trp Pro Thr
850 Val Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly
865 Ala Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn
885 Thr Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu
900 Glu Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met
915 Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly

```

seqlist.txt

```

      930      935      940
Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp
945      950      955
Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr
      965      970      975
Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr
      980      985      990
Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly
      995      1000      1005
Glu Asn Thr Ser Leu Ala His Pro Val Ser Leu His Gly Met Asp Asp
      1010      1015      1020
Pro Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe
1025      1030      1035
His His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr
      1045      1050      1055
Ser Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
      1060      1065      1070
Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
      1075      1080      1085
His Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly
      1090      1095      1100
Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
1105      1110      1115
His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu
      1125      1130      1135
Pro Thr Gly Pro Lys Glu
      1140

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<210> 76
 <211> 3429
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HIV-1 ds-gp120c p17/24 LL-Nef Tatm fusion

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gcgacgcatg cttgcgtgcc tacggacccc aacccccagg aggtgggtgct gggaaacgtg 180
accgagtact tcaacatgtg gaagaataac atgggtggatc agatgcacga ggacatcatc 240
tctctgtggg accagtcctt gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300
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gagggatgtc gccagatcct ggggcaattg cagccatccc tccagaccgg gagtgaagag 1680
ctgaggtcct tgtataacac agtggctacc ctctactgcg tacaccagag gatcgagatt 1740
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seqlist.txt

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<210> 77
 <211> 1142
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HIV-1 ds-gp120c p17/24 LL-Nef Tatm fusion

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35     40     45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50     55     60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65     70     75
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
85     90     95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100    105    110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115    120    125
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130    135    140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145    150    155
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165    170    175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180    185    190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195    200    205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210    215    220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225    230    235    240

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seqlist.txt

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His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Ala	Arg	Lys	Ile	Ile	Gly
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Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Leu	Ser	Arg	Ala	Gln	Trp	Asn	Asn
	305				310					315				320	
Thr	Leu	Lys	Gln	Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys
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Thr	Ile	Lys	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Arg
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His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln
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Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly
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Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met
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Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln
			405						410				415		
Ile	Arg	Cys	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	
			420				425					430			
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro
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Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr
	450					455					460				
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys
	465				470					475				480	
Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly
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Gly	Glu	Leu	Asp	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys
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Gln	Ile	Leu	Gly	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu
	545				550					555				560	
Leu	Arg	Ser	Leu	Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln
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Arg	Ile	Glu	Ile	Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu
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Glu	Gln	Asn	Lys	Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr
		595					600					605			
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	610					615					620				
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Trp	Val	Lys	Val	Val	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	
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Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr
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Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys
		675					680					685			
Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val
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His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser
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Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met
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Thr	Asn	Asn	Pro	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	
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Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile
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Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp
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seqlist.txt

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Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys
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Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met
820 825 830
Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val
835 840 845
Leu Met Gly Gly Lys Trp Ser Ser Ser Val Val Gly Trp Pro Thr
850 855 860
Val Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly
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Ala Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn
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Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr
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<213> Artificial Sequence

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seqlist.txt

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<210> 79

<211> 1141

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 mLL-Nef Tatm fusion

<400> 79

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          20          25          30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
          35          40          45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
          50          55          60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
          65          70          75          80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu

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seqlist.txt

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Asn	Cys	Ser	Phe	Asn	Ile	Thr	Thr	Ser	Ile	Arg	Asp	Lys	Val	Gln	Lys
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Glu	Tyr	Ala	Leu	Phe	Tyr	Asn	Leu	Asp	Val	Val	Pro	Ile	Asp	Asp	Asp
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Asn	Ala	Thr	Thr	Lys	Asn	Lys	Thr	Thr	Arg	Asn	Phe	Arg	Leu	Ile	His
				165					170					175	
Cys	Asn	Ser	Ser	Val	Met	Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe	Glu
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Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	Pro	Ala	Gly	Phe	Ala	Ile	Leu	Lys
		195					200					205			
Cys	Asn	Asn	Lys	Thr	Phe	Asp	Gly	Lys	Gly	Leu	Cys	Thr	Asn	Val	Ser
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Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Arg	Pro	Val	Val	Ser	Thr	Gln	Leu
225					230					235					240
Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	Ile	Arg	Ser	Asp
				245					250					255	
Asn	Phe	Met	Asp	Asn	Thr	Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser
			260					265					270		
Val	Ala	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile
		275					280					285			
His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Ala	Arg	Lys	Ile	Ile	Gly
	290					295					300				
Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Leu	Ser	Arg	Ala	Gln	Trp	Asn	Asn
305					310					315					320
Thr	Leu	Lys	Gln	Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys
				325					330					335	
Thr	Ile	Lys	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Arg
			340					345					350		
His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln
		355					360					365			
Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly
	370					375					380				
Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met
385					390					395					400
Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln
				405					410					415	
Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly
			420					425					430		
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro
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seqlist.txt

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660      665      670
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675      680      685
Glu Thr Ile Asn Glu Glu Ala Glu Trp Asp Arg Val His Pro Val
690      695      700
His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser
705      710      715      720
Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
725      730      735
Thr Asn Asn Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile
740      745      750
Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile
755      760      765
Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp
770      775      780
Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys
785      790      795      800
Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys
805      810      815
Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met
820      825      830
Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val
835      840      845
Leu Met Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val
850      855      860
Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala
865      870      875      880
Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr
885      890      895
Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu
900      905      910
Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
915      920      925
Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
930      935      940
Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
945      950      955      960
Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
965      970      975
Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
980      985      990
Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu
995      1000      1005
Asn Thr Ser Ala Ala His Pro Val Ser Leu His Gly Met Asp Asp Pro
1010      1015      1020
Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
1025      1030      1035      1040
His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser
1045      1050      1055
Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln
1060      1065      1070
Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His
1075      1080      1085
Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg
1090      1095      1100
Lys Lys Arg Arg Gln Arg Arg Pro Pro Gln Gly Ser Gln Thr His
1105      1110      1115      1120
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1125      1130      1135
Thr Gly Pro Lys Glu
1140

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seqlist.txt

<211> 3426
<212> DNA
<213> Artificial Sequence

<220>
<223> HIV-1 ds-gp120c p17/24 mL1-Nef Tatm fusion

<400> 80

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gcgacgcatg	cttgcgtgcc	tacggacccc	aacccccagg	aggtggtgct	gggaaacgtg	180
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tcctatggca	ggaagaagcg	gagacagcga	cgaagacctc	ctcaaggcag	tcagactcat	3360
caagtttctc	tatcaaagca	accaccttc	caatccaaag	gggagccgac	aggcccgaag	3420
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<210> 81

seqlist.txt

<211> 1141

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 mL1-Nef Tatm fusion

<400> 81

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Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
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Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
      35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
      50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65      70      75      80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
      85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
      100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
      115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
      130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145      150      155      160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
      165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
      180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
      195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225      230      235      240
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
      245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Val Gln Leu Asn Glu Ser
      260      265      270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
      275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305      310      315      320
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
      325      330      335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
      340      345      350
His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
      355      360      365
Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly
370      375      380
Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met
385      390      395      400
Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln
      405      410      415
Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
      420      425      430
Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro
      435      440      445
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465      470      475      480

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seqlist.txt

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515 520 525
Arg Phe Ala Val Asn Pro Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg
530 535 540
Gln Ile Leu Gly Gln Leu Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu
545 550 555
Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln
565 570 575
Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu
580 585 590
Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr
595 600 605
Gly His Ser Asn Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile
610 615 620
Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala
625 630 635
Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro
645 650 655
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660 665 670
Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys
675 680 685
Glu Thr Ile Asn Glu Glu Ala Glu Trp Asp Arg Val His Pro Val
690 695 700
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705 710 715
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725 730 735
Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile
740 745 750
Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile
755 760 765
Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp
770 775 780
Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys
785 790 795
Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys
800 805 810
Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met
815 820 825
Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val
830 835 840
Leu Met Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val
845 850 855
Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala
860 865 870
Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr
875 880 885
Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu
890 900 905
Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
910 915 920
Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
925 930 935
Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
940 945 950
Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
955 960 965
Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
970 975 980
Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu
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Asn Thr Ser Ala Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro
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1015 1020

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seqlist.txt

Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
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 Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln
 1060 1065 1070
 Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His
 1075 1080 1085
 Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg
 1090 1095 1100
 Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His
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 Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro
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 1140

<210> 82
 <211> 3426
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HIV-1 ds-gp120c p17/24 mL2-Nef Tatm fusion

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seqlist.txt

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<210> 83

<211> 1141

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 mL2-Nef Tatm fusion

<400> 83

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Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
 35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
 50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
 65      70      75
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
 85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145      150      155
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225      230      235
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Val Gln Leu Asn Glu Ser
260      265      270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305      310      315
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys

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seqlist.txt

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				915						920						925			
				930						935						940			
				945						950						955			
				965						970						975			
				980						985						990			
				995						1000						1005			
				1010						1015						1020			
				1025						1030						1035			
				1045						1050						1055			
				1060						1065						1070			
				1075						1080						1085			
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				1105						1110						1115			
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				1140															

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HIV-1 ds-gp120c RT trNef p17/24 fusion

<400> 84

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<211> 1553

<212> PRT

<213> Artificial Sequence

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<223> HIV-1 ds-gp120c RT trNef p17/24 fusion

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seqlist.txt

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 65 70 75 80
 Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
 85 90 95
 Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
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 Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
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 Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
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seqlist.txt

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 625 630 635 640
 Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu
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seqlist.txt

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gtggtcccca	tcgacgacga	caatgccacc	accaagaaca	agacgacgcg	taatttcaga	3720
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cccgtcgtga	gcacccagct	gctgctgaac	gggtccctgg	ctgaggagga	ggtggtgatc	3960
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seqlist.txt

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gcgattaact gtacccggcc taacaacaac acccgtaagg gcatccacat cgggcctgga 4080
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tcccgcgccc agtggaataa caccctgaag cagatcgtga tcaagctgag agagcacttt 4200
ggaaacaaga ccatcaagtt caatcagagt tctggcggag accccgagat cgtgcggcac 4260
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tggaacggca ccgagggcaa caacacagag ggaaactcca ctatcacctt cccttgccgc 4380
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ggggggccaga tccgctgctc ctccaacatc accggcctgc tgctcaccag agacgggggc 4500
accgagggca acggcacgga gaacgagacg gagatcttca ggcccggcgg cggcgacatg 4560
agggataact ggcggagcga gctgtacaag tacaaggtgg tgaaggtgga gccgctcggc 4620
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<210> 87

<211> 1553

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 RT trNef p17/24 ds gp120c fusion

<400> 87

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Met Gly Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro
1      5      10      15
Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys
20     25     30
Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys
35     40     45
Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala
50     55     60
Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg
65     70     75     80
Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile
85     90     95
Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp
100    105    110
Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys
115    120    125
Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile
130    135    140
Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala
145    150    155    160
Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln
165    170    175
Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly
180    185    190
Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg
195    200    205
Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln
210    215    220
Lys Glu Pro Pro Phe Leu Lys Met Gly Tyr Glu Leu His Pro Asp Lys
225    230    235    240
Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val
245    250    255
Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile
260    265    270
Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr
275    280    285
Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu
290    295    300
Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr
305    310    315    320
Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln
325    330    335
Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys
340    345    350
Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys
355    360    365
Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile

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seqlist.txt

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370      375      380
Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp
385 390 400
Glu Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp
405 415
Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu
420 425 430
Lys Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala
435 440 445
Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly
450 455 460
Arg Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu
465 470 475 480
Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn
485 490 495
Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro
500 505
Asp Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile
515 520 525
Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile
530 535 540
Gly Gly Asn Glu Gln Val Asp Lys Leu Val Ser Ala Gly Ile Arg Lys
545 550 555 560
Val Leu Met Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro
565 570 575
Met Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys
580 585 590
Gly Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu
595 600 605
Asp Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn
610 615 620
Tyr Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys
625 630 635 640
Tyr Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys
645 650 655
Gly Glu Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp
660 665 670
Asp Pro Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala
675 680 685
Phe His His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys
690 695 700
Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
705 710 715 720
Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
725 730 735
His Ile Val Trp Ala Ser Arg Glu Leu Arg Phe Ala Val Asn Pro
740 745 750
Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
755 760 765
Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
770 775 780
Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
785 790 795 800
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Gln Asn Lys Ser Lys
805 810 815
Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val
820 825 830
Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
835 840 845
Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
850 855 860
Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
865 870 875 880
Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
885 890 895
Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
900 905 910
Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala

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seqlist.txt

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Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
930 935 940
Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
945 950 955 960
Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
965 970 975
Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
980 985 990
Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
995 1000 1005
Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
1010 1015 1020
Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
1025 1030 1035 1040
Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
1045 1050 1055
Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Met Ala Glu Gln Leu
1060 1065 1070
Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr
1075 1080 1085
Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His
1090 1095 1100
Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln
1105 1110 1115 1120
Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe Asn Met Trp Lys Asn
1125 1130 1135
Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln
1140 1145 1150
Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asp
1155 1160 1165
Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr Thr Ser Asn Gly
1170 1175 1180
Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
1185 1190 1195 1200
Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys Glu Tyr Ala Leu Phe
1205 1210 1215
Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp Asn Ala Thr Thr Lys
1220 1225 1230
Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His Cys Asn Ser Ser Val
1235 1240 1245
Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His
1250 1255 1260
Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr
1265 1270 1275 1280
Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser Thr Val Gln Cys Thr
1285 1290 1295
His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser
1300 1305 1310
Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp Asn Phe Met Asp Asn
1315 1320 1325
Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Ala Ile Asn Cys
1330 1335 1340
Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly Pro Gly
1345 1350 1355 1360
Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly Asp Ile Arg Gln Ala
1365 1370 1375
His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn Thr Leu Lys Gln Ile
1380 1385 1390
Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys Thr Ile Lys Phe Asn
1395 1400 1405
Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg His Ser Phe Asn Cys
1410 1415 1420
Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln Leu Phe Asn Ser Thr
1425 1430 1435 1440
Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly Asn Ser Thr Ile Thr
1445 1450 1455
Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly

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seqlist.txt

	1460		1465		1470
Lys	Ala	Met	Tyr	Ala	Pro
	1475		1480		1485
Asn	Ile	Thr	Gly	Leu	Leu
	1490		1495		1500
Gly	Thr	Glu	Asn	Glu	Thr
1505			1510		1515
Arg	Asp	Asn	Trp	Arg	Ser
	1525		1530		1535
Glu	Pro	Leu	Gly	Val	Ala
	1540		1545		1550
Arg					

<210> 88
 <211> 2424
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HIV-1 gp120c Nef Tatm fusion

<400> 88

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<210> 89
 <211> 807

seqlist.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 gp120c Nef Tatm fusion

<400> 89

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Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
 35      40      45
Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val
 50      55      60
His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
 65      70      75
Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe Asn Met Trp Lys
 85      90      95
Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
100      105      110
Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
115      120      125
Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr Thr Thr Ser Asn
130      135      140
Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys Asn Cys Ser Phe
145      150      155
Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys Glu Tyr Ala Leu
165      170      175
Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp Asn Ala Thr Thr
180      185      190
Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His Cys Asn Ser Ser
195      200      205
Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
210      215      220
His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys
225      230      235
Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser Thr Val Gln Cys
245      250      255
Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly
260      265      270
Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp Asn Phe Met Asp
275      280      285
Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Ala Ile Asn
290      295      300
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly Pro
305      310      315
Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly Asp Ile Arg Gln
325      330      335
Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn Thr Leu Lys Gln
340      345      350
Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys Thr Ile Lys Phe
355      360      365
Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg His Ser Phe Asn
370      375      380
Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln Leu Phe Asn Ser
385      390      395
Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly Asn Ser Thr Ile
405      410      415
Thr Leu Pro Cys Arg Ile Lys Gln Ile Asn Met Trp Gln Glu Val
420      425      430
Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln Ile Arg Cys Ser
435      440      445
Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Thr Glu Gly
450      455      460
Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp
465      470      475
Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys
480

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seqlist.txt

Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys	Arg	Arg	Val	Val
Gln	Arg	Met	Gly	Gly	Lys	Trp	Ser	Lys	Ser	Ser	Val	Val	Gly	Trp	Pro
Thr	Val	Arg	Glu	Arg	Met	Arg	Arg	Ala	Glu	Pro	Ala	Ala	Asp	Gly	Val
Gly	Ala	Ala	Ser	Arg	Asp	Leu	Glu	Lys	His	Gly	Ala	Ile	Thr	Ser	Ser
Asn	Thr	Ala	Ala	Thr	Asn	Ala	Ala	Cys	Ala	Trp	Leu	Glu	Ala	Gln	Glu
Glu	Glu	Glu	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro
Met	Thr	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys
Gly	Gly	Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu
Asp	Leu	Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn
Tyr	Thr	Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys
Tyr	Lys	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys
Gly	Glu	Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp
Asp	Pro	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala
Phe	His	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys
Thr	Ser	Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	Gly
Ser	Gln	Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys
Phe	His	Cys	Gln	Val	Cys	Phe	Ile	Thr	Ala	Ala	Leu	Gly	Ile	Ser	Tyr
Gly	Arg	Lys	Lys	Arg	Arg	Gln	Arg	Arg	Arg	Pro	Pro	Gln	Gly	Ser	Gln
Thr	His	Gln	Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser	Gln	Ser	Lys	Gly
Glu	Pro	Thr	Gly	Pro	Lys	Glu									

<210> 90
 <211> 2424
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HIV-1 Nef Tatm gp120c fusion

<400> 90					
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caagaggagg	aggaggtggg	ttttccagtc	acacctcagg	tacctttaag	accaatgact 240
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attcactccc	aacgaagaca	agatatcctt	gatctgtgga	tctaccacac	acaaggctac 360
ttccctgatt	ggcagaacta	cacaccaggg	ccaggggtca	gatatccact	gacctttgga 420
tggtgtcata	agctagtacc	agttgagcca	gataaggtag	aagaggccaa	taaaggagag 480
aacaccagct	tgttacaccc	tgtgagcctg	catggaatgg	atgaccctga	gagagaagtg 540
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gagtacttca	agaactgcac	tagtgagcca	gtagatccta	gactagagcc	ctggaagcat 660
ccaggaagtc	agcctaaaaa	tgcttgatcc	aattgctatt	gtaaaaagtg	ttgctttcat 720
tgccaagtgt	gtttcataac	agctgcctta	ggcatctcct	atggcaggaa	gaagcggaga 780
cagcgacgaa	gacctcctca	aggcagtcag	actcatcaag	tttctctatc	aaagcaaccc 840
acctcccaat	ccaaagggga	gccgacaggc	ccgaaggaaa	tgaagggtcaa	ggagaccaga 900
aagaactacc	agcatctgtg	gcgctggggc	accatgctcc	tggaagtgtg	gatgatctgc 960

seqlist.txt

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acgaccaccc tcttctgctg gagcgacgcc aaggcctacg acacggaagt gcataacgtg 1080
tgggcgacgc atgcttgctg gcctacggac cccaaccccc aggaggtggt gctgggaaac 1140
gtgaccgagt acctcaacat gtggaagaat aacatggtgg atcagatgca cgaggacatc 1200
atctctctgt gggaccagtc cctgaagccc tgcgtgaagc tgacgcctct ctgctgaca 1260
ctggactgtg acgacgtcaa caccaccaac agcactacca ccaccagcaa cggctggacc 1320
ggagagattc ggaagggcga gatcaagaac tgctccttca atatcacgac ctcgatcaga 1380
gacaaggtgc agaaggaata cgcgctgttt tataatctcg atgtggtccc catcgacgac 1440
gacaatgcca ccaccaagaa caagacgacg cgtaatttca gactcattca ctgcaacagc 1500
agcgtcatga cgcaggcctg cccaaggtg tccttcgaac caatcccgat ccattactgt 1560
gcccctgccg gattcgcgat cctcaagtgt aacaacaaga ccttcgacgg gaagggcctg 1620
tgcaccaacg tcagcacggt gcagtgcacc catggcatcc gccccgtcgt gagcaccag 1680
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gacaacacca agacaatcat cgtccagctg aacgagctcg tggcgattaa ctgtaccgag 1800
cctaacaaca acaccgtaa gggcatccac atcgggcctg gacgggcctt ctatgccgcc 1860
cgcaagatca tcggcgacat ccggcaggcc cattgcaacc tctcccgcg cagtggaat 1920
aacaccctga agcagatcgt gatcaagctg agagagcact ttggaacaa gaccatcaag 1980
ttcaatcaga gttctggcgg agaccccgag atcgtgcggc actccttcaa ctgagggggc 2040
gagttcttct actcgatcgc gacacagctc ttcaactcca cctggaacgg caccgagggc 2100
aacaacacag agggaaactc cactatcacc ctcccttgcc gcatcaagca gatcatcaac 2160
atgtggcagg aggtgggaaa ggccatgtat gccccccca tcgggggcca gatccgctgc 2220
tcctccaaca tcaccggcct gctgctcacc agagacgggg gcaccgagg caacggcacg 2280
gagaacgaga cggagatctt caggcccggc ggcggcgaca tgagggataa ctggcggagc 2340
gagctgtaca agtacaaggt ggtgaaggtg gagccgctcg gcgtggcccc caccggggcc 2400
aagcgccgcg tcgtgcagag atga 2424
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<210> 91
 <211> 807
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HIV-1 Nef Tatm gp120c fusion

<400> 91
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 20 25 30
 Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Asn Thr
 35 40 45
 Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu
 50 55 60
 Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
 65 70 75 80
 Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
 85 90 95
 Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
 100 105 110
 Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
 115 120 125
 Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
 130 135 140
 Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu
 145 150 155 160
 Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro
 165 170 175
 Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
 180 185 190
 His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser
 195 200 205
 Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln
 210 215 220
 Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His
 225 230 235 240
 Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg
 245 250 255
 Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His

seqlist.txt

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260      265      270
Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro
275      280      285
Thr Gly Pro Lys Glu Met Lys Val Lys Glu Thr Arg Lys Asn Tyr Gln
290      295      300
His Leu Trp Arg Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys
305      310      315
Ser Ala Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
320      325      330
Trp Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala
335      340      345
Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro
350      355      360
Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr
365      370      375
Phe Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile
380      385      390
Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
395      400      405
Leu Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr
410      415      420
Thr Thr Thr Ser Asn Gly Trp Thr Thr Glu Ile Arg Lys Gly Glu Ile
425      430      435
Lys Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln
440      445      450
Lys Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Pro Ile Asp Asp
455      460      465
Asp Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile
470      475      480
His Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe
485      490      495
Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu
500      505      510
Lys Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val
515      520      525
Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln
530      535      540
Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser
545      550      555
Asp Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu
560      565      570
Ser Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly
575      580      585
Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile
590      595      600
Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn
605      610      615
Asn Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn
620      625      630
Lys Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val
635      640      645
Arg His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr
650      655      660
Gln Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu
665      670      675
Gly Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn
680      685      690
Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly
695      700      705
Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp
710      715      720
Gly Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg
725      730      735
Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
740      745      750
Tyr Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala
755      760      765
Lys Arg Arg Val Val Gln Arg
770      775      780
785      790      795
800

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805

<210> 92
 <211> 2232
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HIV-1 trNef Tatm gp120c fusion

<400> 92
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 cgaagacaag atatccttga tctgtggatc taccacacac aaggctactt ccctgattgg 180
 cagaactaca caccagggcc aggggtcaga tatccactga cttttggatg gtgctacaag 240
 ctagtaccag ttgagccaga taaggtagaa gaggccaata aaggagagaa caccagcttg 300
 ttacaccctg tgagcctgca tggaatggat gacctgaga gagaagtgtt agagtggagg 360
 tttgacagcc gcctagcatt tcatcacgtg gcccgagagc tgcattccgga gtacttcaag 420
 aactgcacta gtgagccagt agatcctaga ctagagccct ggaagcatcc aggaagtcat 480
 cctaaaactg cttgtaccaaa ttgctattgt aaaaagtgtt gctttcattg ccaagtttgt 540
 ttcataacag ctgccttagg catctcctat ggcaggaaga agcggagaca gcgacgaaga 600
 cctcctcaag gcagtcagac tcatcaagtt tctctatcaa agcaaccac ctccaatcc 660
 aaaggggagc cgacagggcc gaaggaaatg aagggtcaagg agaccagaaa gaactaccag 720
 catctgtggc gctggggcac catgtccttg ggaatgtga tgatctgctc cgccgccgag 780
 cagctgtggg tcaccgtcta ctacggcgtg cctgtgtgga aggaggccac gaccaccctc 840
 ttctgctgca ggcagcccaa ggcctacgac acggaagtgc ataactgtgt ggcgacgat 900
 gcttgctgca ctacggaccc caaccccag gaggtggtgc tgggaaacgt gaccgagtac 960
 ttcaacatgt ggaagaataa catggtggat cagatgcacg aggacatcat ctctctgttg 1020
 gaccagtccc tgaagccctg cgtgaagctg acgcctctct gcgtgacact ggactgtgac 1080
 gacgtcaaca ccaccaacag cactaccacc accagcaacg gctggaccgg agagattcgg 1140
 aagggcgaga tcaagaactg ctcttcaat atcacgacct cgatcagaga caaggtgcag 1200
 aaggaatacg cgctgtttta taatctcgat gtggtcccca tcgacgacga caatgccacc 1260
 accaagaaca agacgacgca taatttcaga ctcttcaat gcaacagcag cgtcatgacg 1320
 caggcctgcc ccaaggtgtc cttcgaacca atcccgatcc attactgtgc ccctgcccga 1380
 ttctgcgatcc tcaagtgtaa caacaagacc ttcgacggga agggcctgtg caccaacgtc 1440
 agcacggtgc agtgcaccca tggcatccgc cccgtcgtga gcacccagct gctgctgaac 1500
 ggggtccctg ctgaggagga ggtggtgatc cggtcggaca acttcatgga caacaccaag 1560
 acaatcatcg tccagctgaa cgagtctgtg gcgattaact gtacccggcc taacaacaac 1620
 acccgtaagg gcatccacat cgggccttga cgggccttct atgccgcccg caagatcatc 1680
 ggcgacatcc ggcaggccca ttgcaacctc tcccgcgcc agtggaaataa caccctgaag 1740
 cagatcgtga tcaagctgag agagcacttt ggaacaaga ccatcaagtt caatcagagt 1800
 tctggcggag accccgagat cgtgcggcac tccttcaact gcgggggcga gttcttctac 1860
 tgcgatacga cacagctctt caactccacc tggaaacggca ccgagggcaa caacacagag 1920
 ggaaactcca ctatcacctc cccttgccgc atcaagcaga tcatcaacat gtggcaggag 1980
 gtgggaaagg ccattgtatg ccccccatc agggggcaga tccgctgctc ctccaacatc 2040
 accggcctgc tgctcaccag agacgggggc accgagggca acggcacgga gaacgagacg 2100
 gagatcttca ggcccggcgg cggcgacatg agggataact ggcgagcga gctgtacaag 2160
 tacaaggtgg tgaaggtgga gccgctcggc gtggcccca cccgggcaa gcgccgcgtc 2220
 gtgcagagat ga 2232

<210> 93
 <211> 743
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HIV-1 trNef Tatm gp120c fusion

<400> 93
 Met Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
 1 5 10 15
 Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
 20 25 30
 Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
 35 40 45
 Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
 50 55 60

seqlist.txt

Pro 65	Gly	Pro	Gly	Val	Arg 70	Tyr	Pro	Leu	Thr	Phe 75	Gly	Trp	Cys	Tyr	Lys 80
Leu	Val	Pro	Val	Glu 85	Pro	Asp	Lys	Val	Glu 90	Glu	Ala	Asn	Lys	Gly 95	Glu
Asn	Thr	Ser	Leu 100	Leu	His	Pro	Val	Ser 105	Leu	His	Gly	Met	Asp 110	Asp	Pro
Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg 120	Phe	Asp	Ser	Arg	Leu 125	Ala	Phe	His
His	Val 130	Ala	Arg	Glu	Leu	His 135	Pro	Glu	Tyr	Phe	Lys 140	Asn	Cys	Thr	Ser
Glu 145	Pro	Val	Asp	Pro	Arg 150	Leu	Glu	Pro	Trp	Lys 155	His	Pro	Gly	Ser	Gln 160
Pro	Lys	Thr	Ala	Cys 165	Thr	Asn	Cys	Tyr	Cys 170	Lys	Lys	Cys	Cys	Phe 175	His
Cys	Gln	Val	Cys 180	Phe	Ile	Thr	Ala	Ala 185	Leu	Gly	Ile	Ser	Tyr 190	Gly	Arg
Lys	Lys	Arg 195	Arg	Gln	Arg	Arg	Arg 200	Pro	Pro	Gln	Gly	Ser 205	Gln	Thr	His
Gln	Val 210	Ser	Leu	Ser	Lys	Gln 215	Pro	Thr	Ser	Gln	Ser 220	Lys	Gly	Glu	Pro
Thr 225	Gly	Pro	Lys	Glu	Met 230	Lys	Val	Lys	Glu	Thr 235	Arg	Lys	Asn	Tyr	Gln 240
His	Leu	Trp	Arg	Trp 245	Gly	Thr	Met	Leu	Leu 250	Gly	Met	Leu	Met	Ile 255	Cys
Ser	Ala	Ala	Glu 260	Gln	Leu	Trp	Val	Thr 265	Val	Tyr	Tyr	Gly	Val 270	Pro	Val
Trp	Lys	Glu 275	Ala	Thr	Thr	Thr	Leu 280	Phe	Cys	Ala	Ser	Asp 285	Ala	Lys	Ala
Tyr	Asp 290	Thr	Glu	Val	His	Asn 295	Val	Trp	Ala	Thr	His 300	Ala	Cys	Val	Pro
Thr 305	Asp	Pro	Asn	Pro	Gln 310	Glu	Val	Val	Leu	Gly 315	Asn	Val	Thr	Glu	Tyr 320
Phe	Asn	Met	Trp	Lys 325	Asn	Asn	Met	Val	Asp 330	Gln	Met	His	Glu	Asp 335	Ile
Ile	Ser	Leu	Trp 340	Asp	Gln	Ser	Leu	Lys 345	Pro	Cys	Val	Lys	Leu 350	Thr	Pro
Leu	Cys	Val 355	Thr	Leu	Asp	Cys	Asp 360	Asp	Val	Asn	Thr	Thr 365	Asn	Ser	Thr
Thr	Thr 370	Thr	Ser	Asn	Gly	Trp 375	Thr	Gly	Glu	Ile	Arg 380	Lys	Gly	Glu	Ile
Lys 385	Asn	Cys	Ser	Phe	Asn 390	Ile	Thr	Thr	Ser	Ile 395	Arg	Asp	Lys	Val	Gln 400
Lys	Glu	Tyr	Ala	Leu 405	Phe	Tyr	Asn	Leu	Asp 410	Val	Val	Pro	Ile	Asp 415	Asp
Asp	Asn	Ala	Thr 420	Thr	Lys	Asn	Lys	Thr 425	Thr	Arg	Asn	Phe	Arg 430	Leu	Ile
His	Cys	Asn 435	Ser	Ser	Val	Met	Thr 440	Gln	Ala	Cys	Pro	Lys 445	Val	Ser	Phe
Glu	Pro 450	Ile	Pro	Ile	His	Tyr 455	Cys	Ala	Pro	Ala	Gly 460	Phe	Ala	Ile	Leu
Lys 465	Cys	Asn	Asn	Lys	Thr 470	Phe	Asp	Gly	Lys	Gly 475	Leu	Cys	Thr	Asn	Val 480
Ser	Thr	Val	Gln	Cys 485	Thr	His	Gly	Ile	Arg 490	Pro	Val	Val	Ser	Thr 495	Gln
Leu	Leu	Leu	Asn 500	Gly	Ser	Leu	Ala	Glu 505	Glu	Glu	Val	Val	Ile 510	Arg	Ser
Asp	Asn	Phe 515	Met	Asp	Asn	Thr	Lys 520	Thr	Ile	Ile	Val	Gln 525	Leu	Asn	Glu
Ser	Val 530	Ala	Ile	Asn	Cys	Thr 535	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly
Ile 545	His	Ile	Gly	Pro	Gly 550	Arg	Ala	Phe	Tyr	Ala 555	Ala	Arg	Lys	Ile	Ile 560
Gly	Asp	Ile	Arg	Gln 565	Ala	His	Cys	Asn	Leu 570	Ser	Arg	Ala	Gln	Trp 575	Asn
Asn	Thr	Leu	Lys 580	Gln	Ile	Val	Ile	Lys 585	Leu	Arg	Glu	His	Phe 590	Gly	Asn
Lys	Thr	Ile 595	Lys	Phe	Asn	Gln	Ser 600	Ser	Gly	Gly	Asp	Pro 605	Glu	Ile	Val

seqlist.txt

Arg	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr
	610					615					620				
Gln	Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu
625					630					635					640
Gly	Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn
				645					650					655	
Met	Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly
			660					665					670		
Gln	Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp
		675					680					685			
Gly	Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg
	690					695					700				
Pro	Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys
705					710					715					720
Tyr	Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala
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Lys	Arg	Arg	Val	Val	Gln	Arg									
			740												

<210> 94
 <211> 743
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HIV-1 gp120c trNef Tatm fusion

<400> 94

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			20					25					30		
Leu	Trp	Val	Thr	Val	Tyr	Tyr	Gly	Val	Pro	Val	Trp	Lys	Glu	Ala	Thr
		35					40					45			
Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys	Ala	Tyr	Asp	Thr	Glu	Val
	50					55					60				
His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val	Pro	Thr	Asp	Pro	Asn	Pro
65				70					75					80	
Gln	Glu	Val	Val	Leu	Gly	Asn	Val	Thr	Glu	Tyr	Phe	Asn	Met	Trp	Lys
				85					90					95	
Asn	Asn	Met	Val	Asp	Gln	Met	His	Glu	Asp	Ile	Ile	Ser	Leu	Trp	Asp
		100						105					110		
Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val	Thr	Leu
		115					120					125			
Asp	Cys	Asp	Asp	Val	Asn	Thr	Thr	Asn	Ser	Thr	Thr	Thr	Thr	Ser	Asn
	130					135					140				
Gly	Trp	Thr	Gly	Glu	Ile	Arg	Lys	Gly	Glu	Ile	Lys	Asn	Cys	Ser	Phe
145					150					155					160
Asn	Ile	Thr	Thr	Ser	Ile	Arg	Asp	Lys	Val	Gln	Lys	Glu	Tyr	Ala	Leu
				165					170					175	
Phe	Tyr	Asn	Leu	Asp	Val	Val	Pro	Ile	Asp	Asp	Asp	Asn	Ala	Thr	Thr
		180						185					190		
Lys	Asn	Lys	Thr	Thr	Arg	Asn	Phe	Arg	Leu	Ile	His	Cys	Asn	Ser	Ser
		195					200					205			
Val	Met	Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe	Glu	Pro	Ile	Pro	Ile
	210					215					220				
His	Tyr	Cys	Ala	Pro	Ala	Gly	Phe	Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys
225					230					235					240
Thr	Phe	Asp	Gly	Lys	Gly	Leu	Cys	Thr	Asn	Val	Ser	Thr	Val	Gln	Cys
				245					250					255	
Thr	His	Gly	Ile	Arg	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly
			260					265					270		
Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	Ile	Arg	Ser	Asp	Asn	Phe	Met	Asp
		275					280					285			
Asn	Thr	Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser	Val	Ala	Ile	Asn
	290					295					300				
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile	His	Ile	Gly	Pro

seqlist.txt

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305          310          315          320
Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly Asp Ile Arg Gln
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          340          345          350
Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys Thr Ile Lys Phe
          355          360          365
Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg His Ser Phe Asn
          370          375          380
Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln Leu Phe Asn Ser
          385          390          395
Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly Asn Ser Thr Ile
          405          410          415
Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val
          420          425          430
Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln Ile Arg Cys Ser
          435          440          445
Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Thr Glu Gly
          450          455          460
Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp
          465          470          475
Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys
          485          490          495
Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Val Val
          500          505          510
Gln Arg Met Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro
          515          520          525
Met Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys
          530          535          540
Gly Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu
          545          550          555
Asp Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn
          565          570          575
Tyr Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys
          580          585          590
Tyr Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys
          595          600          605
Gly Glu Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp
          610          615          620
Asp Pro Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala
          625          630          635
Phe His His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys
          645          650          655
Thr Ser Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly
          660          665          670
Ser Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys
          675          680          685
Phe His Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr
          690          695          700
Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Gln Gly Ser Gln
          705          710          715
Thr His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly
          725          730          735
Glu Pro Thr Gly Pro Lys Glu
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<210> 95

<211> 1971

<212> DNA

<213> Artificial sequence

<220>

<223> HIV-1 gp120c trNef fusion

<400> 95

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ctgggaatgc tgatgatctg ctccgccgcc gagcagctgt gggtcaccgt ctactacggc 120

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seqlist.txt

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<210> 96

<211> 656

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 gp120c trNef fusion

<400> 96

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Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
 35          40          45
Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val
 50          55          60
His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
 65          70          75          80
Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe Asn Met Trp Lys
 85          90          95
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100          105          110
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115          120          125
Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr Thr Ser Asn
130          135          140
Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys Asn Cys Ser Phe
145          150          155          160
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165          170          175
Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp Asn Ala Thr Thr
180          185          190
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seqlist.txt

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<211> 3060
<212> DNA
<213> Artificial Sequence
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<220>
<223> HIV-1 gp120c p17/24 trNef fusion

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<210> 98
 <211> 1019
 <212> PRT
 <213> Artificial sequence

<220>
 <223> HIV-1 gp120c p17/24 trNef fusion

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 35 40 45
 Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val
 50 55 60

seq1ist.txt

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seqlist.txt

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<211> 3321

<212> DNA

<213> Artificial Sequence

<220>

<223> HIV-1 gp120c p17/24 trNef Tatm fusion

<400> 99

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seqlist.txt

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<212> PRT

<213> Artificial Sequence

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<223> HIV-1 gp120c p17/24 trNef Tatm fusion

<400> 100

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Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
          35          40          45
Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val

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seqlist.txt

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					85		Gln	Met	His	Glu	Asp	90	Ile	Ile	Ser	Leu	95	Trp	Asp
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	Phe	Tyr	Asn	Leu	180	Asp	Val	Val	Pro	Ile	Asp	185	Asp	Asp	Asp	Asn	Ala	Thr	Thr
	Lys	Asn	Lys	Thr	Thr	Arg	Asn	Phe	200	Arg	Leu	Ile	His	Cys	205	Asn	Ser	Ser	
	Val	Met	Thr	Gln	Ala	Cys	Pro	Lys	215	Val	Ser	Phe	Glu	Pro	Ile	Pro	Ile		
	His	Tyr	Cys	Ala	Pro	Ala	230	Gly	Phe	Ala	Ile	Leu	235	Lys	Cys	Asn	Asn	Lys	240
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	Ser	Leu	Ala	Glu	Glu	Val	Val	Ile	Arg	Ser	Asp	Asn	285	Phe	Met	Asp			
	Asn	Thr	Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser	300	Val	Ala	Ile	Asn		
	Cys	Thr	Arg	Pro	Asn	Asn	310	Asn	Thr	Arg	Lys	Gly	315	Ile	His	Ile	Gly	Pro	320
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	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln	445	Ile	Arg	Cys	Ser		
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	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	540	Lys	Lys	Tyr	Lys		
	Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	555	Arg	Phe	Ala	Val	560	
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	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu			
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seqlist.txt

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645 650 655
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660 665 670
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675 680 685
Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr
690 695 700
Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn
705 710 715 720
Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro
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740 745 750
Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro
755 760 765
Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu
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785 790 795 800
Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys
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865 870 875 880
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915 920 925
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930 935 940
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Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser
965 970 975
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980 985 990
Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His His Val Ala
995 1000 1005
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seqlist.txt

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seqlist.txt

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 His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
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 85 90 95
 Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
 100 105 110
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 115 120 125
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 130 135 140
 Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys Asn Cys Ser Phe
 145 150 155 160
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 Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp Asn Ala Thr Thr
 180 185 190
 Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His Cys Asn Ser Ser
 195 200 205
 Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
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 370 375 380
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seqlist.txt

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755      760      765
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945      950      955      960
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Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr
980      985      990
His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro
995      1000      1005
Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro

```

seqlist.txt

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1010      1015      1020
Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser
1025      1030      1035      1040
Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu
1045      1050      1055
Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His His Val Ala
1060      1065      1070
Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser Glu Pro Val
1075      1080      1085
Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln Pro Lys Thr
1090      1095      1100
Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His Cys Gln Val
1105      1110      1115      1120
Cys Phe Ile Thr Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys Arg
1125      1130      1135
Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His Gln Val Ser
1140      1145      1150
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1155      1160      1165
Lys Glu
1170

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<210> 103
 <211> 3513
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HIV-1 gp120c p17/24 mL1-Nef Tatm fusion

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<400> 103
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gacacggaag tgcataacgt gtgggcgacg catgcttgcg tgcctacgga cccaacccc 240
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seqlist.txt

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<210> 104

<211> 1170

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 gp120c p17/24 mL1-Nef Tatm fusion

<400> 104

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Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
 35      40      45
Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val
 50      55      60
His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
 65      70      75      80
Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe Asn Met Trp Lys
 85      90      95
Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
100      105      110
Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
115      120      125
Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr Thr Ser Asn
130      135      140
Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys Asn Cys Ser Phe
145      150      155      160
Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys Glu Tyr Ala Leu
165      170      175
Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp Asn Ala Thr Thr
180      185      190
Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His Cys Asn Ser Ser
195      200      205
Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
210      215      220
His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys
225      230      235      240
Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser Thr Val Gln Cys
245      250      255
Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly
260      265      270
Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp Asn Phe Met Asp

```

seqlist.txt

Asn	Thr	Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser	Val	Ala	Ile	Asn
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Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile	His	Ile	Gly	Pro
305					310					315					320
Gly	Arg	Ala	Phe	Tyr	Ala	Ala	Arg	Lys	Ile	Ile	Gly	Asp	Ile	Arg	Gln
				325					330					335	
Ala	His	Cys	Asn	Leu	Ser	Arg	Ala	Gln	Trp	Asn	Asn	Thr	Leu	Lys	Gln
			340					345					350		
Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys	Thr	Ile	Lys	Phe
		355					360					365			
Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Arg	His	Ser	Phe	Asn
	370					375					380				
Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln	Leu	Phe	Asn	Ser
385					390					395					400
Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly	Asn	Ser	Thr	Ile
				405					410					415	
Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Asn	Met	Trp	Gln	Glu	Val	
			420					425				430			
Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln	Ile	Arg	Cys	Ser
		435					440					445			
Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	Gly	Thr	Glu	Gly
	450					455					460				
Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro	Gly	Gly	Gly	Asp
465					470				475						480
Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Lys
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Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys	Arg	Arg	Val	Val
			500					505					510		
Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly	Gly	Glu	Leu	Asp
		515					520					525			
Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	Lys	Tyr	Lys
	530					535					540				
Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Val
545					550					555					560
Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly
				565					570					575	
Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu
			580					585					590		
Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Glu	Ile
		595					600					605			
Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Glu	Gln	Asn	Lys
	610					615					620				
Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	His	Ser	Asn
625					630					635					640
Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met
				645					650					655	
Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val
			660					665					670		
Val	Glu	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala
		675					680					685			
Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr
	690					695					700				
Val	Gly	Gly	His	Gln	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	
705					710					715					720
Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro
				725					730					735	
Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly
			740					745					750		
Thr	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro
		755					760					765			
Pro	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu
	770					775					780				
Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg
785					790					795					800
Gln	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys
				805					810					815	
Thr	Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr

seqlist.txt

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 835 840 845
 Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys
 850 855 860
 Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Met Gly Gly
 865 870 875 880
 Lys Trp Ser Lys Ser Val Val Gly Trp Pro Thr Val Arg Glu Arg
 885 890 895
 Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala Ala Ser Arg
 900 905 910
 Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr Ala Ala Thr
 915 920 925
 Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu Glu Val Gly
 930 935 940
 Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala
 945 950 955 960
 Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly
 965 970 975
 Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr
 980 985 990
 His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro
 995 1000 1005
 Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro
 1010 1015 1020
 Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser
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 Ala Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu
 1045 1050 1055
 Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His His Val Ala
 1060 1065 1070
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 1075 1080 1085
 Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln Pro Lys Thr
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 Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His Cys Gln Val
 1105 1110 1115 1120
 Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys Arg
 1125 1130 1135
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 1170

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 <211> 3204
 <212> DNA
 <213> Artificial sequence

<220>
 <223> HIV-1 RT Nef p17/24 fusion

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seqlist.txt

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<210> 106

<211> 1067

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 RT Nef p17/24 fusion

<400> 106

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25      30      35      40      45
Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys
50      55      60      65      70
Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala
75      80      85      90      95
Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg
100     105     110     115     120
Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile
125     130     135     140     145
Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp
150     155     160     165     170
Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys
175     180     185     190     195

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seqlist.txt

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145 150 155
Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln
165 170 175
Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly
180 185 190
Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Leu Arg
195 200 205
Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln
210 215 220
Lys Glu Pro Pro Phe Leu Lys Met Gly Tyr Glu Leu His Pro Asp Lys
225 230 235
Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val
245 250 255
Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile
260 265 270
Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr
275 280 285
Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu
290 295 300
Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr
305 310 315
Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln
325 330 335
Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys
340 345 350
Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys
355 360 365
Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile
370 375 380
Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp
385 390 395
Glu Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp
405 410 415
Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu
420 425 430
Lys Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala
435 440 445
Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly
450 455 460
Arg Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu
465 470 475
Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn
485 490 495
Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro
500 505 510
Asp Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile
515 520 525
Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile
530 535 540
Gly Gly Asn Glu Gln Val Asp Lys Leu Val Ser Ala Gly Ile Arg Lys
545 550 555
Val Leu Met Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro
565 570 575
Met Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys
580 585 590
Gly Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu
595 600 605
Asp Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn
610 615 620
Tyr Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys
625 630 635
Tyr Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys
645 650 655
Gly Glu Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp
660 665 670

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seqlist.txt

Asp	Pro	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala
		675					680					685			
Phe	His	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys
		690				695					700				
Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly	Gly	Glu	Leu	Asp	Arg	Trp
705					710					715					720
Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	Lys	Tyr	Lys	Leu	Lys
				725					730					735	
His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Val	Asn	Pro
			740					745					750		
Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly	Gln	Leu
		755					760					765			
Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu	Tyr	Asn
		770				775					780				
Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Glu	Ile	Lys	Asp
785					790					795					800
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Gln	Asn	Lys	Ser	Lys	
				805					810					815	
Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	His	Ser	Asn	Gln	Val
			820					825					830		
Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met	Val	His
		835					840					845			
Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu
		850				855					860				
Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser
865					870					875					880
Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly
				885					890					895	
Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu
			900					905					910		
Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala
		915					920					925			
Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr
		930				935					940				
Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro	Ile
945					950					955					960
Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys
				965					970					975	
Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly
			980					985					990		
Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	Leu
		995					1000					1005			
Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr
						1015					1020				
Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	Ala
1025					1030					1035					1040
Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly
				1045					1050					1055	
Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val	Leu					
			1060					1065							